SEQUENCE LISTING

<110> CARILLO, Serge

BLANCHARD, Jean-Marie PIECHACZYK, Marc <120> METHOD OF CANCER TREATMENT BY P53 PROTEIN CONTROL <130> ST94037A-US <140> <141> <150> 08/737,953 <151> 1996-11-27 <150> FR94/06583 <151> 1994-05-31 <150> WO PCT/FR95/00670 <151> 1995-05-22 <160> 4 <170> PatentIn Ver. 2.1 <210> 1 <211> 2085 <212> DNA <213> Homo sapiens <220> <221> CDS ..<222> (1)..(2085) <400> 1 atg gaa gga cca cat ctt cct aac aag aaa aaa cac aaa aaa cag gct Met Glu Gly Pro His Leu Pro Asn Lys Lys Lys His Lys Lys Gln Ala 1 10 15 gta aaa aca gaa cct gag aag aag tca cag tca acc aag ctg tct gtg Val Lys Thr Glu Pro Glu Lys Lys Ser Gln Ser Thr Lys Leu Ser Val 20 30 gtt cat gag aaa aaa tcc caa gaa gga aag cca aaa gaa cac aca gag 144 Val His Glu Lys Lys Ser Gln Glu Gly Lys Pro Lys Glu His Thr Glu 35 45 40 cca aaa agc cta ccc aag cag gca tca gat aca gga agt aac gat gct 192 Pro Lys Ser Leu Pro Lys Gln Ala Ser Asp Thr Gly Ser Asn Asp Ala 50 55 60 cac aat aaa aaa gca gtt tcc aga tca gct gaa cag cag cca tca gag 240 His Asn Lys Lys Ala Val Ser Arg Ser Ala Glu Gln Gln Pro Ser Glu 65 70 80 75 aaa tca aca gaa cca aag act aaa cca caa gac atg att tct gct ggt 288 Lys Ser Thr Glu Pro Lys Thr Lys Pro Gln Asp Met Ile Ser Ala Gly

90 95

				l Ala					Ile			_	_	Gly	gac Asp	336
			Gli					Thr					Val	_	tct Ser	384
		Asp					Lys	tca Ser				Ala		· -	gat Asp	432
	Leu					Gly		cct Pro			Thr					480
					Pro		=	tca Ser	_	Pro	_	_				528
Ile	Glu	Glu	Leu 180	Gly	Lys	Arg	Glu	Val 185	Thr	Ile	Pro	Pro	Lys 190	Tyr		
Glu	Leu	Leu 195	Ala	Lys	Lys	Glu	Gly 200	atc	Thr	Gly	Pro	Pro 205	Ala	Asp	Ser	624
Ser	Lys 210	Pro	Ile	Gly	Pro	Asp 215	Asp	Ala	Ile	Asp	Ala 220	Leu	Ser	Ser	_	
Phe 225	Thr	Cys	Gly	Ser	Pro 230	Thr	Ala	Ala	Gly	Lys 235	Lys	Thr	Glu	Lys	240	-
Glu	Ser	Thr	Glu	Val 245	Leu	Lys	Ala	Cag Gln	Ser 250	Ala	Gly	Thr	Val	Arg 255	Ser	768
Ala	Ala	Pro	Pro 260	Gln	Glu	Lys	Lys	Arg 265	Lys	Val	Glu	Lys	Asp 270	Thr		
Ser	Asp	Gln 275	Ala	Leu	Glu	Ala	Leu 280	tcg Ser	Ala	Ser	Leu	Gly 285	Thr	Arg	Gln	864
Ala	Glu 290	Pro	Glu	Leu	Asp	Leu 295	Arg	tca Ser	Ile	Lys	Glu 300	Val	Asp	Glu	Ala	912
				Glu				aag Lys	Cys							960

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•	•			•	1				•										
-						r Arg					a Thi					a aaa / Lys	1008		
					o Gl					Pro					Glu	tca Ser	1056		
	gaa Glu	t cto	ati i Ile 35	e As	t gaa	a ctt ı Lei	tca Ser	gaa Glu 360	Asp	ttt Phe	gac Asp	cgg Arg	tct Ser 365	Glu	tgt Cys	aaa Lys	1104		
			s Pro					Glu					Ser			gct	1152		
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	Ile	Gln	Ser	· Ala	405	Pro	Glu	Pro	Ala	Thr 410	Leu	Lys	Gly	Thr	Val 415		1248		
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	Pro 465	Asp	Tyr	Arg	Leu	Glu 470	Glu	gtc Val	Lys	Asp	Lys 475	Asp	Gly	Lys	Pro	Leu 480	1440		
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	Ser	Leu	Lys 515	Phe	Glu	Asp	Ala	aaa Lys 520	Leu	Ala	Ala	Ala	Ile 525	Ser	Glu	Val	1584	·	
	gtt Val	ser 530	caa Gln	acc Thr	cca Pro	Ala	tca Ser 535	acg a	acc Thr	caa Gln	Ala	gga Gly 540	gcc Ala	cca Pro	ccc Pro	cgt Arg	1632		
	gat Asp																1680		

545					550	1			555				560	
			cta Lev		Gln				Pro				cca Pro	1728
			aaa Lys 580	Val				Lys					aag Lys	1776
			aga Arg										ctg Leu	1824
_	_		gga Gly	_				=			_ ·		tca Ser	1872
			aag Lys											1920
		– .	ctg Leu		Ser	_				_		_		1968
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Lys Lys Lys Glu Lys Lys Ser Leu Thr Pro Ala Val Pro Val Glu Ser Lys Pro Asp Lys Pro Ser Gly Lys Ser Gly Met Asp Ala Ala Leu Asp Asp Leu Ile Asp Thr Leu Gly Gly Pro Glu Glu Thr Glu Glu Glu Asn Thr Thr Tyr Thr Gly Pro Glu Val Ser Asp Pro Met Ser Ser Thr Tyr Ile Glu Glu Leu Gly Lys Arg Glu Val Thr Ile Pro Pro Lys Tyr Arg Glu Leu Leu Ala Lys Lys Glu Gly Ile Thr Gly Pro Pro Ala Asp Ser Ser Lys Pro Ile Gly Pro Asp Asp Ala Ile Asp Ala Leu Ser Ser Asp Phe Thr Cys Gly Ser Pro Thr Ala Ala Gly Lys Lys Thr Glu Lys Glu Glu Ser Thr Glu Val Leu Lys Ala Gln Ser Ala Gly Thr Val Arg Ser Ala Ala Pro Pro Gln Glu Lys Lys Arg Lys Val Glu Lys Asp Thr Met Ser Asp Gln Ala Leu Glu Ala Leu Ser Ala Ser Leu Gly Thr Arg Gln Ala Glu Pro Glu Leu Asp Leu Arg Ser Ile Lys Glu Val Asp Glu Ala Lys Ala Lys Glu Glu Lys Leu Glu Lys Cys Gly Glu Asp Asp Glu Thr Ile Pro Ser Glu Tyr Arg Leu Lys Pro Ala Thr Asp Lys Asp Gly Lys Pro Leu Pro Glu Pro Glu Glu Lys Pro Lys Pro Arg Ser Glu Ser Glu Leu Ile Asp Glu Leu Ser Glu Asp Phe Asp Arg Ser Glu Cys Lys Glu Lys Pro Ser Lys Pro Thr Glu Lys Thr Glu Glu Ser Lys Ala Ala Ala Pro Ala Pro Val Ser Glu Ala Val Ser Arg Thr Ser Met Cys Ser Ile Gln Ser Ala Pro Pro Glu Pro Ala Thr Leu Lys Gly Thr Val Pro Asp Asp Ala Val Glu Ala Leu Ala Asp Ser Leu Gly Lys Lys Glu Ala Asp Pro Glu Asp Gly Lys Pro Val Met Asp Lys Val Lys Glu Lys Ala Lys Glu Glu Asp Arg Glu Lys Leu Gly Glu Lys Glu Glu Thr Ile Pro Pro Asp Tyr Arg Leu Glu Glu Val Lys Asp Lys Asp Gly Lys Pro Leu Leu Pro Lys Glu Ser Lys Glu Gln Leu Pro Pro Met Ser Glu Asp Phe Leu Leu Asp Ala Leu Ser Glu Asp Phe Ser Gly Pro Gln Asn Ala Ser Ser Leu Lys Phe Glu Asp Ala Lys Leu Ala Ala Ala Ile Ser Glu Val Val Ser Gln Thr Pro Ala Ser Thr Thr Gln Ala Gly Ala Pro Pro Arg Asp Thr Ser Gln Ser Asp Lys Asp Leu Asp Asp Ala Leu Asp Lys Leu Ser Asp Ser Leu Gly Gln Arg Gln Pro Asp Pro Asp Glu Asn Lys Pro

				565					570					575	
Met	Gly	Asp	Lys 580		Lys	Glu	Lys	Ala 585	Lys	Ala	Glu	His	Arg 590	Asp	Lys
Leu	Gly	Glu 595	Arg	Asp	Asp	Thr	Ile 600	Pro	Pro	Glu	Tyr	Arg 605	His	Leu	Leu
Asp	Asp 610	Asn	Gly	Gln	Asp	Lys 615	Pro	Val	Lys	Pro	Pro 620	Thr	Lys	Lys	Ser
Glu 625	Asp	Ser	Lys	Lys	Pro 630	Ala	Asp	Asp	Gln	Asp 635	Pro	Ile	Asp	Ala	Leu 640
Ser	Gly	Asp	Leu	Asp 645	Ser	Cys	Pro	Ser	Thr 650	Thr	Glu	Thr	Ser	Gln 655	Asn
Thr	Ala	Lys	Asp 660	Lys	Cys	Lys	Lys	Ala 665	Ala	Ser	Ser	Ser	Lys 670	Ala	Pro
Lys	Asn	Gly 675	Gly	Lys	Ala	Lys	Asp 680	Ser	Ala	Lys	Thr	Thr 685	Glu	Glu	Thr
Ser	Lys 690	Pro	Lys	Asp	Asp										
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	Gly	Met	Asp		Ala	Leu	Asp	Asp		Ile	Asp	Thr	Leu		Gly	••
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Pro	GIU	GIU		GIU	GIU	GIU	Asn		Thr	Tyr	Thr	GIÀ		Glu	Val	
			20					25					30			
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															gaa	144
ser	Asp								Glu					Arg	GIU	
		35					40					45				
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									cta			_				192
vaı		TIE	PIO	PIO	пåр		Arg	GIU	Leu	ren		Lys	тĀг	GIU	GIA	
	50					55					60					
ato	202	~~~	cct	cat	aa.	a a a	+ ~+	+ ==		000	242	~~~	0.00			240
									aaa					_	_	240
TTE	111T	GT A	PIO	PLO	WIG	Asp	SEL	ser	Lys	PIO	TTG	GTA	PIO	Asp	Asp	

gct ata gac gcc ttg tca tct gac ttc acc tgt ggg tcg cct aca gct Ala Ile Asp Ala Leu Ser Ser Asp Phe Thr Cys Gly Ser Pro Thr Ala gct gga aag aaa act gaa aaa gag gaa tct aca gaa gtt tta aaa gct Ala Gly Lys Lys Thr Glu Lys Glu Glu Ser Thr Glu Val Leu Lys Ala

cag tca gca ggg aca gtc aga agt gct gct cca ccc caa gag aag aaa 384 Gln Ser Ala Gly Thr Val Arg Ser Ala Ala Pro Pro Gln Glu Lys Lys 115 120 125

aga aag gtg gag aag Arg Lys Val Glu Lys 130

399

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Ser Asp Pro Met Ser Ser Thr Tyr Ile Glu Glu Leu Gly Lys Arg Glu
35 40 45

Val Thr Ile Pro Pro Lys Tyr Arg Glu Leu Leu Ala Lys Lys Glu Gly
50 60

Ile Thr Gly Pro Pro Ala Asp Ser Ser Lys Pro Ile Gly Pro Asp Asp65707580

Ala Ile Asp Ala Leu Ser Ser Asp Phe Thr Cys Gly Ser Pro Thr Ala 85 90 95

Ala Gly Lys Lys Thr Glu Lys Glu Glu Ser Thr Glu Val Leu Lys Ala 100 105 110

Gln Ser Ala Gly Thr Val Arg Ser Ala Ala Pro Pro Gln Glu Lys Lys 115 120 125

Arg Lys Val Glu Lys 130